Amendments to the Specification:

Please replace the paragraph beginning at page 8, line 14, with the following amended paragraph:

Figures 21a and 21b shows a phylogenetic analysis of terpene synthases of known function and shows that alpha-farnesene synthase forms a unique clade.

Please replace the paragraph beginning at page 11, line 21, with the following amended paragraph:

A polynucleotide or polypeptide sequence may be aligned, and the percentage of identical nucleotides in a specified region may be determined against another sequence, using computer algorithms that are publicly available. Two exemplary algorithms for aligning and identifying the similarity of polynucleotide sequences are the BLASTN and FASTA algorithms. The similarity of polypeptide sequences may be examined using the BLASTP algorithm. Both the BLASTN and BLASTP software are available on the NCBI anonymous FTP server ~~(ftp://ncbi.nlm.nih.gov) under /blast/executables/~~. The BLASTN algorithm version 2.0.4 [Feb-24-1998], set to the default parameters described in the documentation of variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN and BLASTP, is described at NCBI's website ~~at URL~~ http://www.ncbi.nlm.nih.gov/BLAST/newblast.html and in the publication of Altschul et al., Nucleic Acids Res. 25, 3389-34023 (1997). The computer algorithm FASTA is available on the Internet ~~at the ftp site ftp://ftp.virginia.edu/pub/fasta/~~. Version 2.0u4, February 1996, set to the default parameters described in the documentation and distributed with the algorithm, is also preferred for use in the determination of variants according to the present invention. The use of the FASTA algorithm is described in Pearson and Lipman Proc. Natl. Acad. Sci. USA 85, 2444-2448 (1988), Pearson Methods in Enzymology 183, 63-98 (1990).

Please replace the paragraph beginning at page 41, line 3, with the following amended paragraph:

Computational analysis was performed using the European Molecular Biology Open Software Suite (EMBOSS) (Rice et al., 2000). Sequence identity and similarity was calculated using the pair wise alignment program Needle, which uses the algorithm of Needleman and Wunsch (J. Mol. Biol. 48; 443-453 (1970). The default parameters were used (Gap extension penalty: 0.5 for any sequence; Gap opening penalty: 10 for any sequence). Sequence relatedness was analysed using CLUSTAL X and trimmed and shaded using the program GeneDoc (Nicholas and Nicholas, 1997). Phylogenetic trees were used generated in CLUSTAL X using the neighbour-joining method, and the uprooted trees visualised using Treedraw ~~(http://taxonomy.zoology.gla.ac.us/rod/treeview.html; Page 1996)~~.

Please replace the paragraph beginning at page 41, line 13, with the following amended paragraph:

The full length alpha-farnesene synthase was compared to all other terpene synthase sequences of known function (Figures 21a and 21b). It formed a clade with a single member, well separated from the nearest homologues, two isoprene synthases from poplar. The separation into its own group reinforces the dissimilarity of the protein sequence to both other sesquiterpene synthases and to monoterpene synthases. A similar result was obtained when only the active site metal binding region around the DDxxD motif was compared across the same set of sequences. In short, this gene would not have been predicted to be a sesquiterpene synthase.